Nirenberg History Code Cracked

The Code is Cracked!

This period, between 1961 and 1962, is often referred to as the “coding race” because of the competition between Ochoa's and Nirenberg's labs. Indeed, the two laboratories completed the base composition part of the code almost simultaneously. However, Ochoa’s laboratory stopped working on the problem when they realized how close Nirenberg and his colleagues were to completing the sequencing.

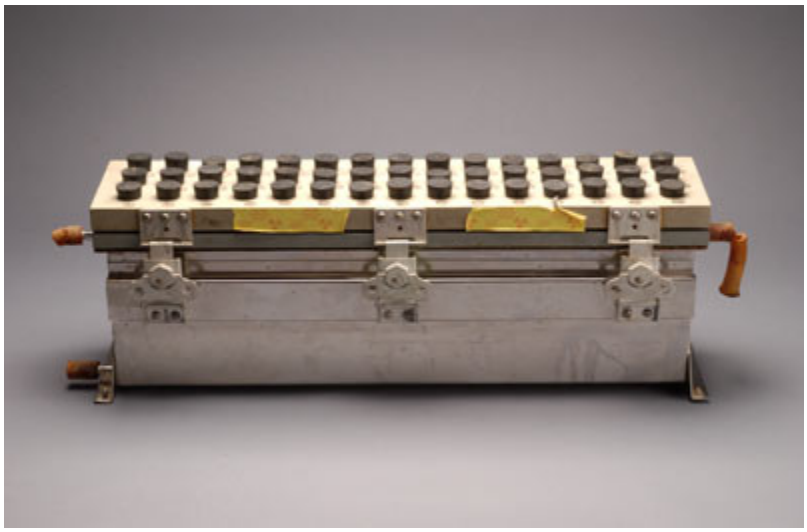
Several scientific instruments proved necessary in the long years from 1961-1965 while dozens of people toiled in Nirenberg's lab. The French press and the multi-plater were only two examples of instruments that helped save time and solve problems. In the years when the laboratory was devoted to sequencing the bases in each codon, these instruments were of vital importance to getting the work done. The innovation of scientists and laboratory technicians who worked with Nirenberg helped a great deal.

By 1965, Nirenberg, with help from his NIH colleagues, had become the first to complete the sequencing of the code. The language of DNA was understood. Once completely solved, the genetic code could be expressed in a chart. By looking up the sequence of nucleotide bases, readers could identify the resulting amino acid. To read the code, select a letter from the left, right, and top columns, such as U-C-A. This combination represents an mRNA codon. Draw imaginary horizontal and vertical lines to connect the letters. They intersect at the amino acid for which they code. For example, UCA is the code for serine.

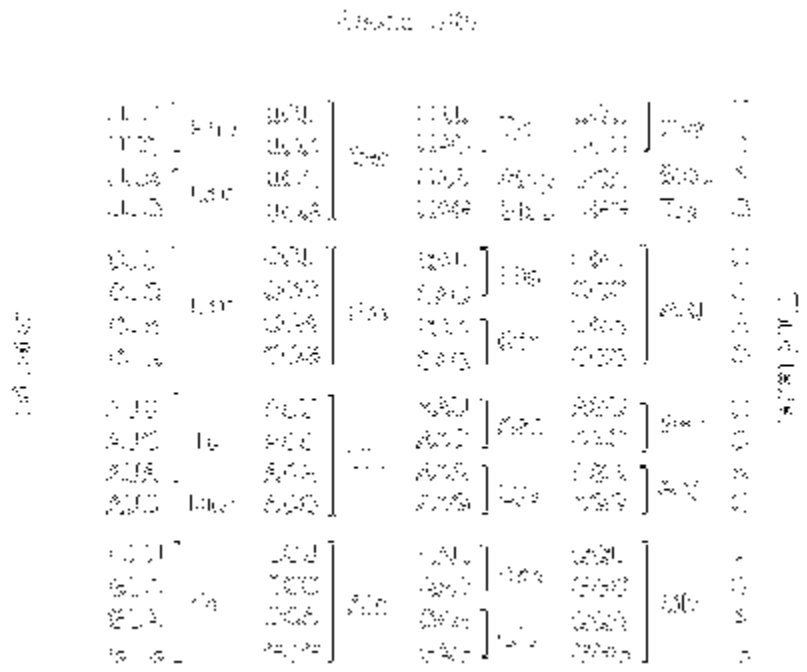
The genetic code has seven main characteristics:

1. It is made up of codons, which are triplets of bases. Each codon specifies a specific amino acid.
2. The codons do not overlap; that is, the sequence GCCCAC contains two triplets, “GCC” and “CAC” not counting the “CCC” and other subsequent three-letter sequences.
3. The code includes punctuation in the form of three “stop” codons that do not code for an amino acid: UAA, UAG, and UGA.
4. The genetic code is known as a “degenerate” code. This means that each amino acid is triggered by between one and six codons. (There are only 20 amino acids and 64 possible codon triplets).
5. To read each gene and glean the necessary information to form proteins, cells begin at a fixed and particular starting point on the mRNA strand. The initiation codon is AUG (methionine).
6. The mRNA strand is read from the 5' to the 3' end.
7. If there are mutations or errors in the DNA, the message may be changed and incorrect protein formation results.

French press



Multi-plater



The completed chart of the genetic code